

Table S4. Top genes enriched in “Un Gfp+” population.

Shaded *sub1* mutant was identified in this study as having higher basal *pFUS1*-GFP reporter expression.

Systematic Name	Common Name	Log2 Fold Change	padj	Individually Tested Phenotype	Newly Made Mutant Phenotype
YNL049C	SFB2	5.652	1.38E-08	Wild-type	
YDR391C	YDR391C	5.497	3.24E-07		
YOR378W	YOR378W	5.311	1.38E-12	Wild-type	
YDL197C	ASF2	5.242	2.00E-06		
YCL025C	AGP1	5.130	2.28E-05		
YOR342C	YOR342C	5.109	1.88E-06	Wild-type	
YBR090C	YBR090C	4.936	3.75E-09	Wild-type	
YNL299W	TRF5	4.853	9.27E-06	No Induction	Wild-type
YOR093C	YOR093C	4.836	2.83E-07	Wild-type	
YIL136W	OM45	4.832	1.42E-06	Wild-type	
YBL063W	KIP1	4.721	3.54E-11	Wild-type	
YJR019C	TES1	4.496	1.74E-08	Lower basal	Wild-type
YLL015W	BPT1	4.331	7.07E-06	Wild-type	
YNL271C	BNI1	3.935	6.11E-61	Higher basal; higher induced	
YDR192C	NUP42	3.663	3.72E-18		
YOR279C	RFM1	3.559	3.77E-67		
YLL047W	YLL047W	3.521	6.14E-09	Wild-type	
YPL248C	GAL4	3.497	1.86E-07		
YLR064W	PER33	3.460	3.76E-09		
YPR031W	NTO1	3.458	9.32E-06		
YLR093C	NYV1	3.417	1.22E-05		
YOL068C	HST1	3.323	1.75E-06		
YGL254W	FZF1	3.321	4.49E-07	Wild-type	
YER053C	PIC2	3.238	1.62E-10		
YPL246C	RBD2	3.122	5.07E-08		
YMR039C	SUB1	3.122	0.0033	Higher basal	Higher basal